Amendments to the Specification:

Please replace paragraph [0087] with the following paragraph:[1]

[0087] The examination of databases, such as are made available, for example, by <u>the</u> EMBL website (see Toolbox at the EBI) ~~(http://www.ebi.ac.uk/Tools/index.htm)~~ or <u>the</u> NCBI (National Center for Biotechnology Information, ~~http://www.ncbi.nlm.nih.gov/~~) <u>website</u>, can also be used for identifying homologous sequences, which code for OK1 protein. In this case, one or more sequences are specified as a so-called query. This query sequence is then compared by means of statistical computer programs with sequences, which are contained in the selected databases. Such database queries (e.g. blast or fasta searches) are known to the person skilled in the art and can be carried out by various providers.

Please replace paragraph [0088] with the following paragraph:

[0088] If such a database query is carried out, e.g. at the NCBI (National Center for Biotechnology Information, ~~http://www.ncbi.nlm.nih.gov/~~) <u>website</u>, then the standard settings, which are specified for the particular comparison inquiry, should be used. For protein sequence comparisons (blastp), these are the following settings: Limit entrez=not activated; Filter=low complexity activated; Expect value=10; word size=3; Matrix=BLOSUM62; Gap costs: Existence=11, Extension=1.

Please replace paragraph [0337] with the following paragraph:

[0337] Identification of the amino acid sequence of proteins, which have increased bonding activity with respect to P-starch in comparison with non-phosphorylated starch Proteins identified in accordance with Step a) are digested with trypsin and the peptides obtained are analysed by means of MALDI-TOF to determine the masses of the peptides obtained. Trypsin is a sequence-specific protease, i.e. trypsin only splits proteins at a specified position when the proteins concerned contain certain amino acid sequences. Trypsin always splits peptide bonds when the amino acids arginine and lysine follow one another starting from the N-terminus. In this way, it is possible to theoretically determine all peptides that would be produced following the trypsin digestion of an amino acid sequence. From the knowledge

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[1] All paragraph numbers cited herein refer to the paragraph numbers set forth in U.S. US 2008/0022421 ("the '421 publication"), the publication of the instant application.

of the amino acids coding the theoretically determined peptides, the masses of the peptides, which are obtained after theoretical trypsin digestion, can also be determined. Databases (e.g. Protein Prospector and Swissprot websites ~~NCBInr~~ ~~http://prospector.ucsf.edu/ucsfhtml4.0/msfit.htm;~~ ~~Swissprot~~ ~~http://cbrg.inf.ethz.ch/Server/MassSearch.html~~), which contain information concerning the masses of peptides after theoretical trypsin digestion, can therefore be compared with the real masses of peptides of unknown proteins obtained with MALDI-TOF-MS. Amino acid sequences, which have the same peptide masses after theoretical and/or real trypsin digestion, are to be looked upon as being identical. The databases concerned contain both peptide masses of proteins, the function of which has already been shown, and also peptide masses of proteins, which up to now only exist hypothetically by derivation from amino acid sequences starting from nucleic acid sequences obtained in sequencing projects. The actual existence and the function of such hypothetical proteins has therefore seldom been shown and, if there is a function at all, then this is usually based only on predictions and not on an actual demonstration of the function.

Please replace paragraph [0398] with the following paragraph:

[0398] The band of the protein with a molecular weight of ca. 130 kDa identified in Step e) was excised from the gel. The protein was subsequently released from the acrylamide as described under General Methods, Item 10b, digested with trypsin and the peptide masses obtained were determined by means of MALD-TOF-MS. The so-called "fingerprint" obtained by MALDI-TOF-MS was compared with fingerprints of theoretically digested amino acid molecules in databases (See the Mascot, ~~:~~ ~~http://www.matrixscience.com/search_form_select.html;~~ ~~ProFound,~~ and ~~:~~ ~~http://29.85.19.192/profound_bin/WebProFound.exe;~~ ~~PepSea:~~ ~~http://195.41.108.38/PepSeaIntro.html~~ websites). As such a fingerprint is very specific to a protein, it was possible to identify an amino acid molecule. With the help of the sequence of this amino acid molecule, it was possible to isolate a nucleic acid sequence from Arabidopsis thaliana coding an OK1 protein. The protein identified with this method was designated as A.t.-OK1. Analysis of the amino acid sequence of the OK1 protein from Arabidopsis thaliana showed that this deviated from the sequence that was present in the database (NP 198009, NCBI). The amino acid sequence shown in SEQ ID No 2 codes the A.t.-OK1

protein. SEQ ID No 2 contains deviations when compared with the sequence in the database (Acc.: NP 198009.1, NCBI). The amino acids 519 to 523 (WRLCE) and 762 to 766 (VRARQ) contained in SEQ ID No 2 are not in the sequence, which is present in the database (ACC.: NP 198009.1). Compared with Version 2 of the database sequence (Acc.: NP 198009.2), the amino acid sequence shown in SEQ ID NO 2 also contains the additional amino acids 519 to 523 (WRLCE).

Please replace paragraph [0499] with the following paragraph:

[0499] pMCS5 (Mobitec website, ~~www.mobitec.de~~) was digested with BgIII and BamHI and re-inserted. The plasmid contained was designated as pML4.

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